

C Nucleocapsid Assembly

Caposio, P., Gillespie, ME., Streblow, DN.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

03/05/2024

Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

This document contains 1 reaction ([see Table of Contents](#))

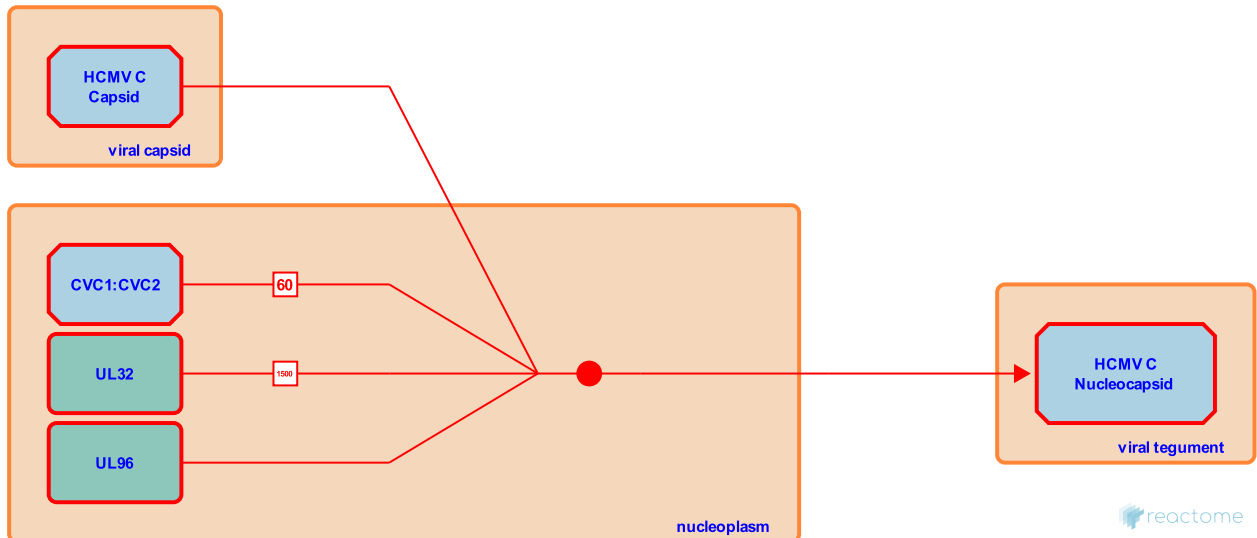
C Nucleocapsid Assembly [↗](#)

Stable identifier: R-HSA-9698931

Type: binding

Compartments: nucleoplasm

Diseases: viral infectious disease



An infectious C capsid acquires both tegument and transport protein in the nucleus. A putative capsid vertex capping complex (CVC), composed of UL77 (CVC1) and UL93 (CVC2) proteins, decorates penton tips, and the UL51 and UL52 proteins are added to provide capsid stability. The order of addition of capsid vertex and stabilizing proteins (UL77, UL93, UL51, and UL52) remains to be established. It is not yet resolved whether these proteins are to be considered components of the capsid or tegument. The most capsid-proximal major tegument protein in HCMV is the UL32 protein, pp150, added to nucleocapsids in the nucleus and accompanying maturing particles to the cytoplasm. The pp150 and ppUL96 proteins stabilize nucleocapsids in a common pathway of translocation to cytoplasmic sites of envelopment.

Literature references

Knipe, DM., Howley, PM. (2013). Chapter 62 - Cytomegaloviruses, Fields Virology. *Lippincott Williams & Wilkins*.

Editions

2019-10-18	Reviewed	Streblov, DN., Caposio, P.
2019-11-12	Authored, Edited	Gillespie, ME.